



X16758M Final Sequence Feb 2008.ST25.txt  
SEQUENCE LISTING

<110> Watkins, Jeffry D.  
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Huse, William D.

<120> TNF-alpha Binding Molecules

<130> X-16758M

<140> PCT/US04/00290

<141> 2004-01-08

<150> 10/338,552

<151> 2003-01-08

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<151> 2003-01-08

<160> 122

<170> PatentIn version 3.3

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Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Ser Ser  
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile  
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala  
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85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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 aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240  
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 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu  
 50 55 60  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser  
 65 70 75 80  
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr  
 85 90 95  
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 Gly Thr Leu Val Thr Val Ser Ser  
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Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Tyr Ser  
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile  
35 40 45

Lys Tyr Ala Ser Glu Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala  
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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gatcagtcctc caaagctcct catcaagtat gcttctgagt ctagggtctgg ggtcccctcg 180

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ser Asn His  
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Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Gly Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu  
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln  
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cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca 240  
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Arg Ala Ser Gln Phe val Gly Met Ser Ile His  
 Page 5

1 5 10

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tatgcttctg agtctatgtc t

21

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<400> 22

tatgcttctg agtatatgtc t

21

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21

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Tyr Ala Ser Glu Ser Arg Ser  
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<210> 26

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<400> 26

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21

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Tyr Ala Ser Glu Ser Lys Ser  
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<210> 28

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<400> 28

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21

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21

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Gln Gln Ser His Ser Trp His Phe Thr  
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27

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Gly Phe Thr Phe Ser Asn His Trp Met Asn  
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Gly Phe Lys Phe Ser Asn His Trp Met Asn  
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Gly Phe Pro Phe Ser Asn His Trp Met Asn  
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Val Lys Gly

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<400> 44  
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Val Lys Gly

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Val Lys Gly

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Val Lys Gly

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Val Lys Gly

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Val Lys Gly

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<400> 57

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Glu Lys Val Thr Ile Thr Cys  
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<400> 58

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<210> 59  
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<400> 59

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Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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<210> 61  
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atcacctgc 69

<210> 62  
<211> 45  
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<400> 62  
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<400> 64  
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<400> 65  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser  
20 25

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<210> 67  
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<400> 67  
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1 5 10 15

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
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<212> PRT  
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 1 5 10

<210> 69  
 <211> 75  
 <212> DNA  
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 tcctgtgcag cctct 75

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<210> 71  
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Arg Ala Pro Gln Phe Val Gly Ser Ser Ile His  
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<400> 77
Arg Ala Ser Gln Phe Val Tyr Ser Ser Ile His
1 5 10

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 <222> (19)..(21)  
 <223> The nucleotides in these positions could be any nucleotides

<400> 80  
 agggccagtc agttcgttnn ntcaagcatc cac 33

<210> 81  
 <211> 9  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 81  
 Gln Gln Ser His Trp Trp His Phe Thr  
 1 5

<210> 82  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 82  
 caacaaagtc attggtggca tttcacg

<210> 83  
<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> The residue in this position could be any amino acid

<400> 83

Gln Gln Ser His Xaa Trp His Phe Thr  
1 5

<210> 84  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Synthetic Construct

<220>  
<221> misc\_feature  
<222> (13)..(15)  
<223> The nucleotides in these positions could be any nucleotides

<400> 84  
caacaaagtc atnnntggca tttcacg 27

<210> 85  
<211> 357  
<212> DNA  
<213> Homo sapiens

<400> 85  
tcagcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 60  
gggggacacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 120  
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 180  
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcaccacg 240  
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagcagag 300  
cccaaattct ctactagtgt tctctaccca tatgatgtac ctgattatgc atcatag 357

<210> 86  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 86  
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60

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ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag	120
tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac	180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag	240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag	300
agcttcaaca ggggagagtc ttag	324

<210> 87  
 <211> 10  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 87

Gly	Phe	Thr	Phe	Arg	Asn	His	Trp	Met	Asn
1				5					10

<210> 88  
 <211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 88 ggattcactt tccggaacca ctggatgaac	30
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<210> 89  
 <211> 19  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 89

Glu	Ile	Arg	Ser	Lys	Ser	Ile	Asn	Ser	Ala	Thr	Phe	Tyr	Ala	Glu	Ser
1				5					10					15	

val Lys Gly

<210> 90  
 <211> 57  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 90 gaaattagat caaaatctat taattctgca acattttatg cggagtctgt gaaaggg	57
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<210> 91  
 <211> 9  
 <212> PRT  
 <213> Artificial

<220>  
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<400> 91

Asn Tyr Tyr Gly Ser Tyr Tyr Asp His  
 1 5

<210> 92  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 92  
 aattactacg gtagttatta cgaccat

27

<210> 93  
 <211> 11  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 93

Val Thr Thr Gln Phe Val Gly Tyr Ala Ile His  
 1 5 10

<210> 94  
 <211> 33  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 94  
 gttactactc agttcgttgg ctatgctatc cac

33

<210> 95  
 <211> 7  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 95

Tyr Ala Ser Ser Ser Arg Ser  
 1 5

<210> 96

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<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 96  
tatgcttctt cgtctaggtc t

21

<210> 97  
<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 97

Gln Gln Ser His Gly Trp Pro Phe Thr  
1 5

<210> 98  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 98  
caacaaagtc atgggtggcc tttcacg

27

<210> 99  
<211> 10  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 99

Gly Phe Lys Phe Arg Asn His Trp Met Asn  
1 5 10

<210> 100  
<211> 30  
<212> DNA  
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<220>  
<223> Synthetic Construct

<400> 100  
ggattcaagt tccgtaacca ctggatgaac

30

<210> 101  
<211> 10  
<212> PRT  
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<220>

<223> Synthetic Construct

<400> 101

Gly Phe Asp Phe Arg Asn His Trp Met Asn  
1 5 10

<210> 102

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 102

ggattcgatt tccggaacca ctggatgaac

30

<210> 103

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 103

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr Phe Tyr Ala Glu Ser  
1 5 10 15

val Lys Gly

<210> 104

<211> 57

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 104

gaaattagat caaaatctat gaattctgca acattttatg cggagtctgt gaaaggg

57

<210> 105

<211> 11

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 105

Ala Ala Ser Gln Phe val Gly Gln Ala Ile His  
1 5 10

<210> 106

<211> 33  
 <212> DNA  
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 <223> Synthetic Construct  
 <400> 106  
 gcggcttctc agttcgttgg ccaggcgatc cac 33

<210> 107  
 <211> 7  
 <212> PRT  
 <213> Artificial  
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 <223> Synthetic Construct  
 <400> 107

Tyr Ala Asn Glu Ser Arg Ser  
 1 5

<210> 108  
 <211> 21  
 <212> DNA  
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 <223> Synthetic Construct  
 <400> 108  
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<210> 109  
 <211> 39  
 <212> DNA  
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 <223> Synthetic Construct  
 <400> 109  
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<210> 110  
 <211> 21  
 <212> DNA  
 <213> Artificial  
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 <223> Synthetic Construct  
 <400> 110  
 tggctcccag gtgccaaatg t 21

<210> 111  
 <211> 21  
 <212> DNA  
 <213> Artificial  
 <220>

&lt;223&gt; Synthetic Construct

&lt;400&gt; 111

gacagatggg gcagccacag t

21

&lt;210&gt; 112

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 112

ctctccacag gtgtccactc ccagggtccaa ctgcaggtc

39

&lt;210&gt; 113

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 113

ctctccacag gtgtccactc c

21

&lt;210&gt; 114

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 114

gaagaccgat gggcccttgg t

21

&lt;210&gt; 115

&lt;211&gt; 450

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 115

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn His  
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr Phe Tyr Ala Glu  
 50 55 60

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Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser  
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr  
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Tyr Tyr Asp His Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg  
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Lys  
450

<210> 116  
<211> 213  
<212> PRT  
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<220>  
<223> Synthetic Construct

<400> 116

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Val Thr Thr Gln Phe Val Gly Tyr Ala  
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Tyr Ala Ser Ser Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His Gly Trp Pro Phe  
85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
195 200 205

Asn Arg Gly Glu Cys  
210

<210> 117  
<211> 39  
<212> DNA  
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<220>  
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<400> 117  
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39

<210> 118  
<211> 21  
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<213> Artificial

<220>  
<223> Synthetic Construct

<400> 118  
tggctcccag gtgccaaatg t

21

<210> 119  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 119  
gacagatggt gcagccacag t

21

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<210> 120  
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<220>  
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<400> 120  
 ctctccacag gtgtccactc ccagggtccaa ctgcaggtc 39

<210> 121  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 121  
 ctctccacag gtgtccactc c 21

<210> 122  
 <211> 21  
 <212> DNA  
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<220>  
 <223> Synthetic Construct

<400> 122  
 gaagaccgat gggcccttgg t 21